# MultiQC

v1.12
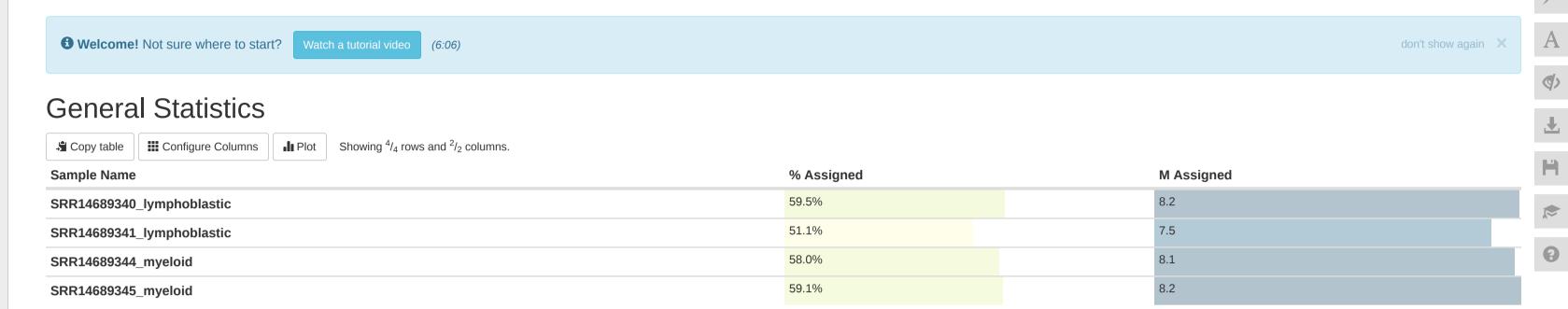
General Stats

featureCounts

A modular tool to aggregate results from bioinformatics analyses across many samples into a single report.

ℹ **Welcome!** Not sure where to start?   Watch a tutorial video   *(6:06)*                                                                                          don't show again ✕

## General Statistics

📋 Copy table    ▦ Configure Columns    📊 Plot    Showing ⁴/₄ rows and ²/₂ columns.

| Sample Name | % Assigned | M Assigned |
|---|---|---|
| **SRR14689340_lymphoblastic** | 59.5% | 8.2 |
| **SRR14689341_lymphoblastic** | 51.1% | 7.5 |
| **SRR14689344_myeloid** | 58.0% | 8.1 |
| **SRR14689345_myeloid** | 59.1% | 8.2 |

## featureCounts

Subread featureCounts is a highly efficient general-purpose read summarization program that counts mapped reads for genomic features such as genes, exons, promoter, gene bodies, genomic bins and chromosomal locations.   *DOI: 10.1093/bioinformatics/btt656.*

Number of Reads    Percentages

### featureCounts: Assignments

⬇ Export Plot



● Assigned   ● Unassigned: Mapping Quality   ● Unassigned: No Features   ● Unassigned: Ambiguity

Created with MultiQC

SciLifeLab

Toolbox